

Figure 1

00000000000000000000

Figure 2

2562T680

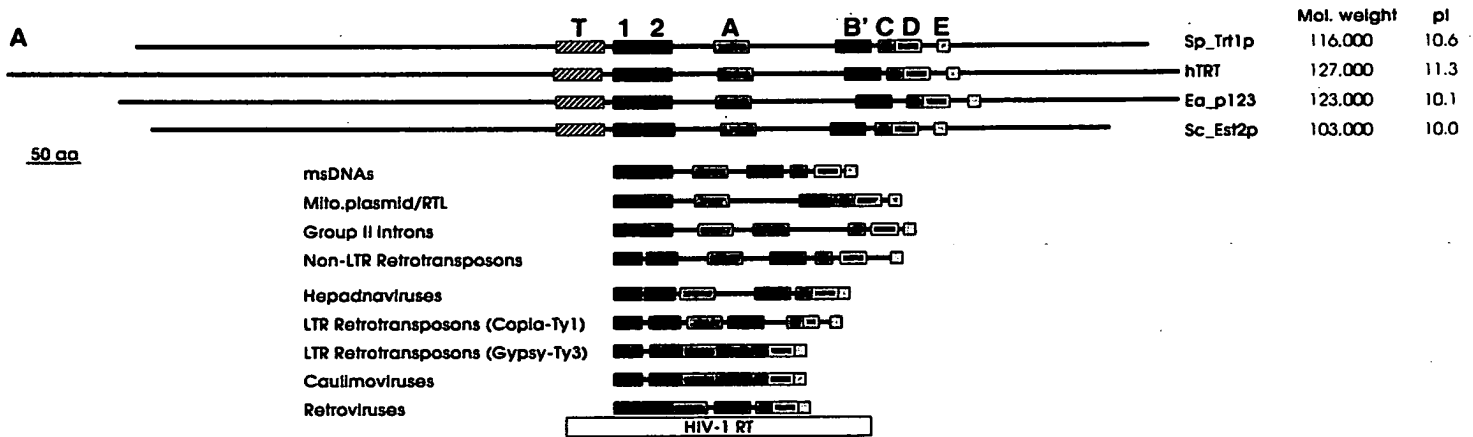
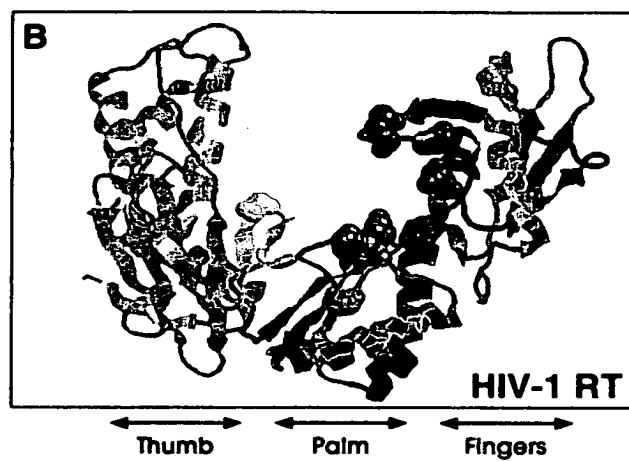
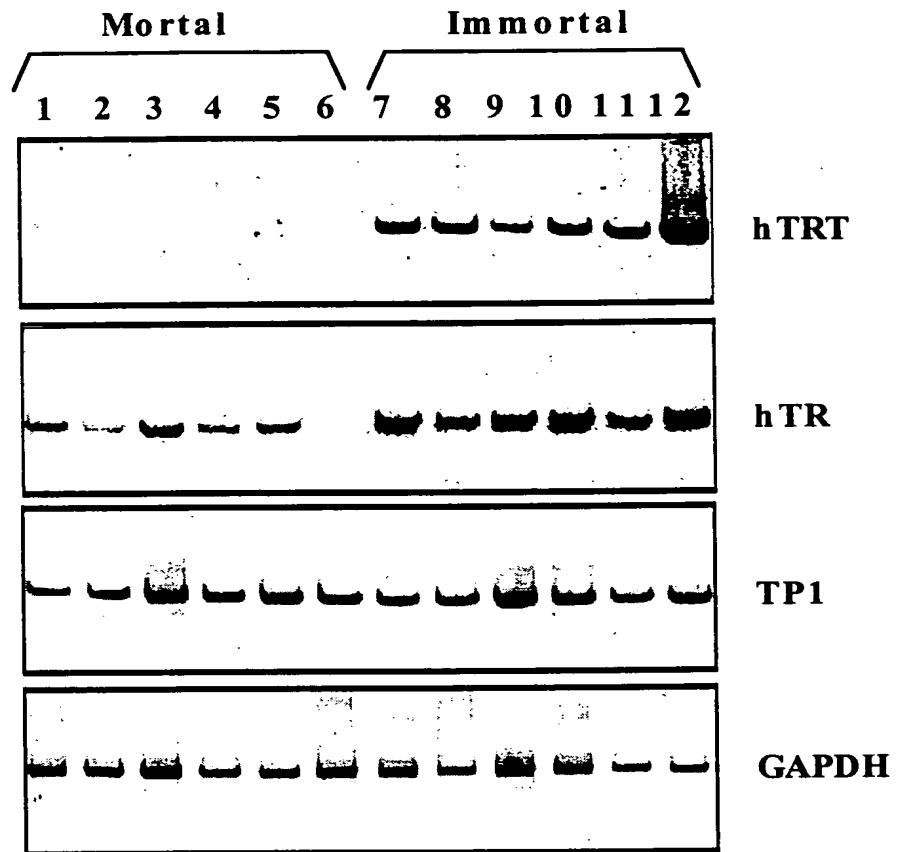


Figure 3



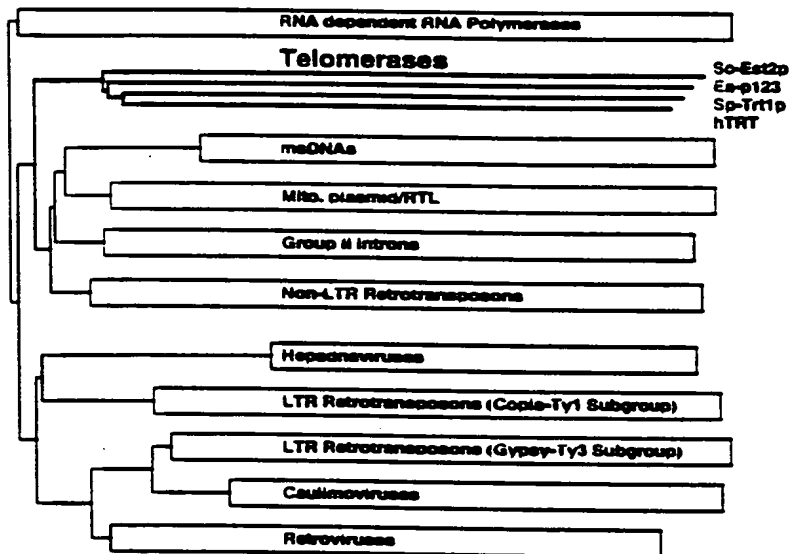
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Figure 5



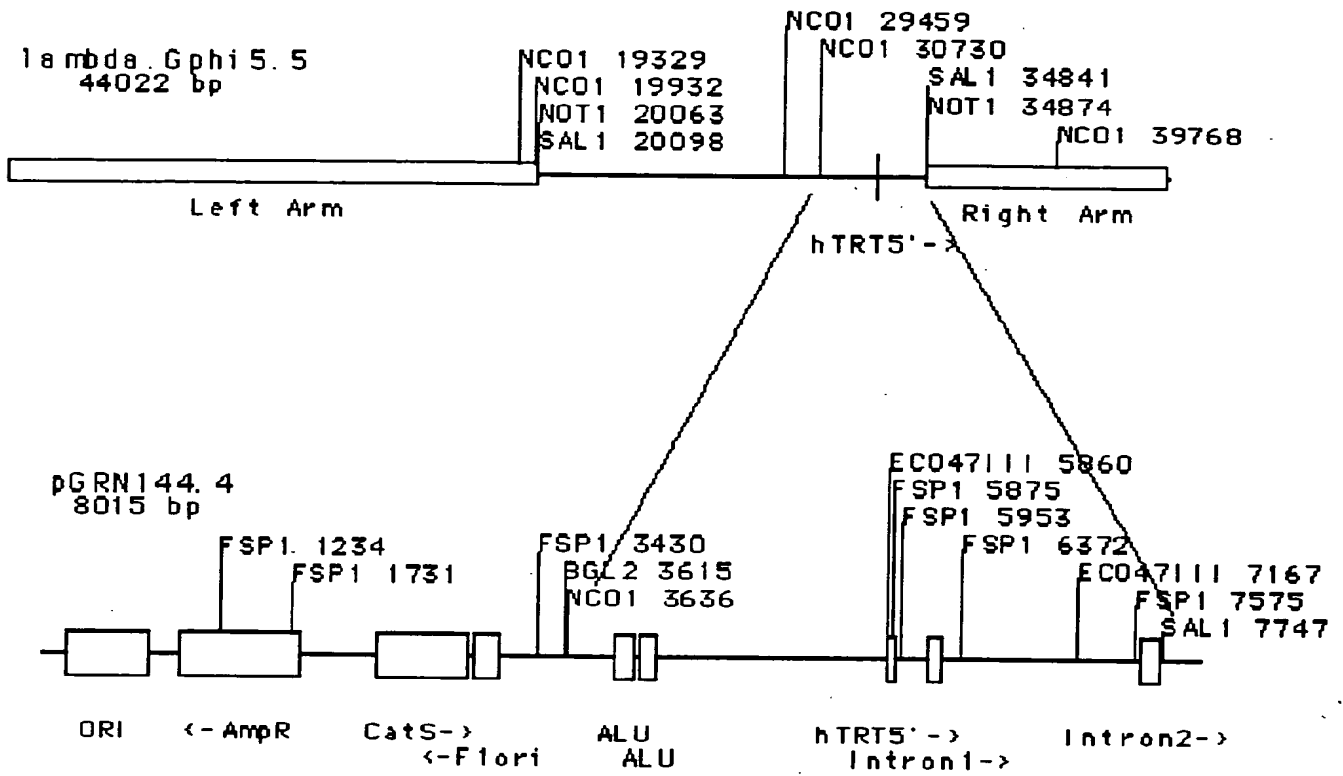
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Figure 6



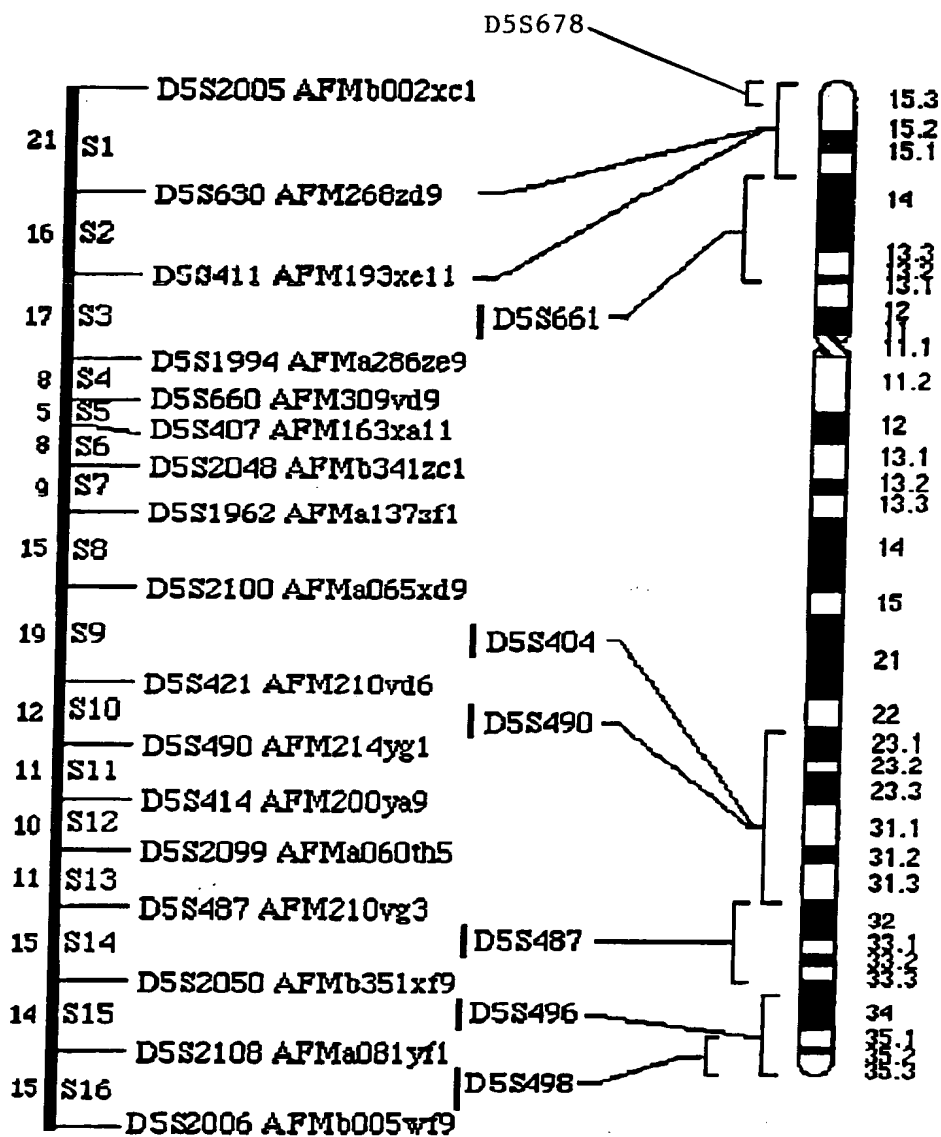
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Figure 7



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Figure 8



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FIGURE 9

Promoter Reporter Construct

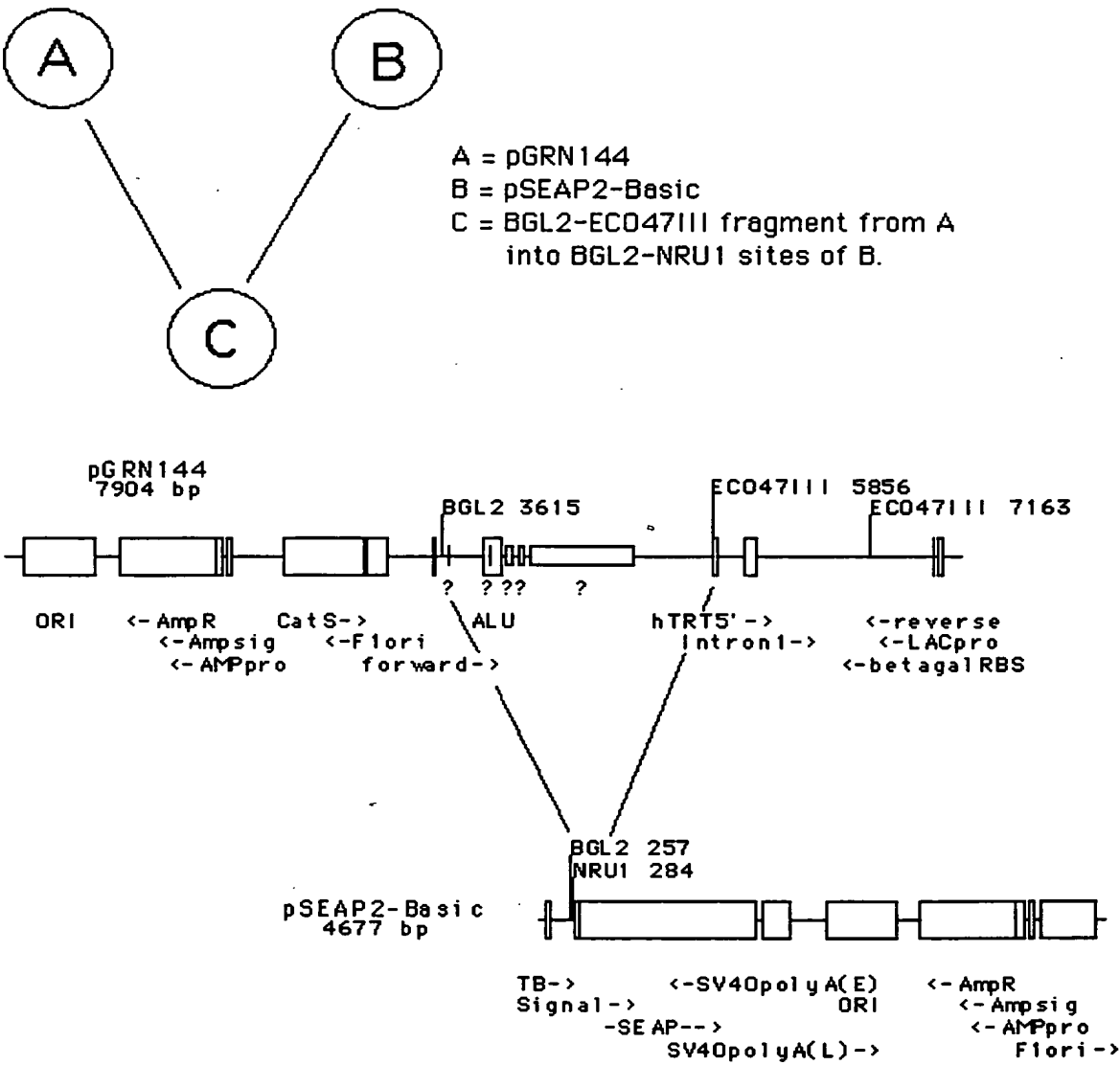
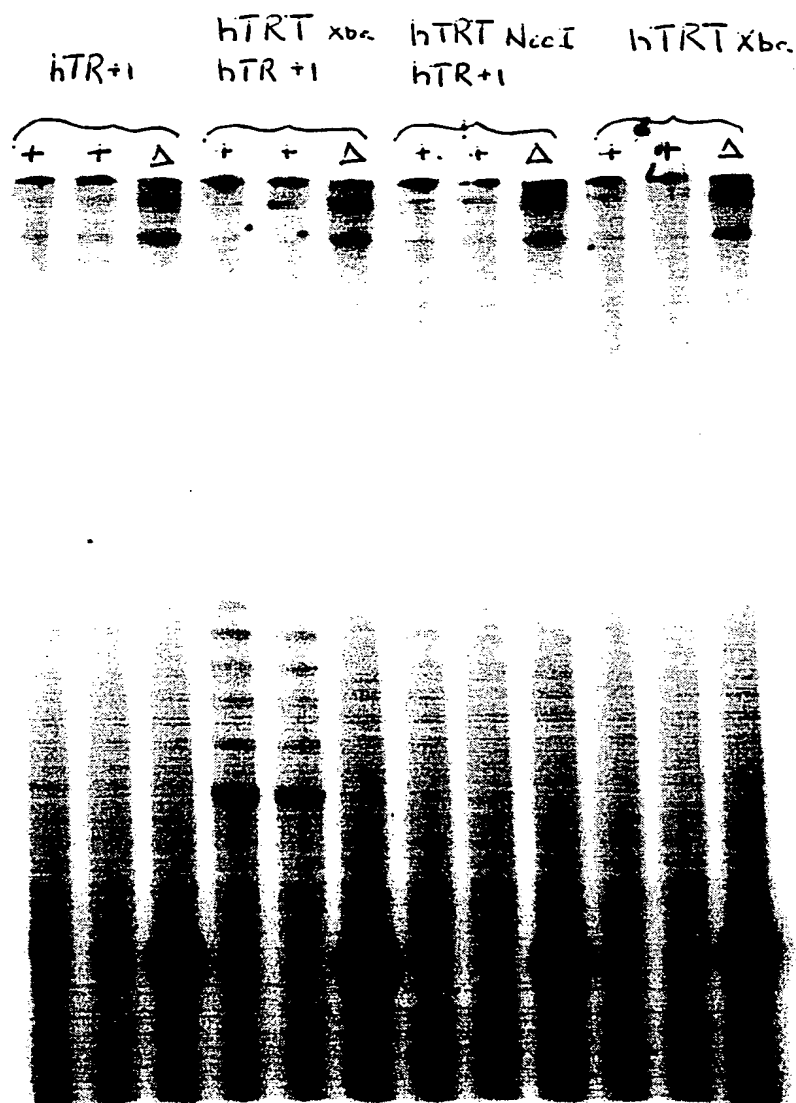
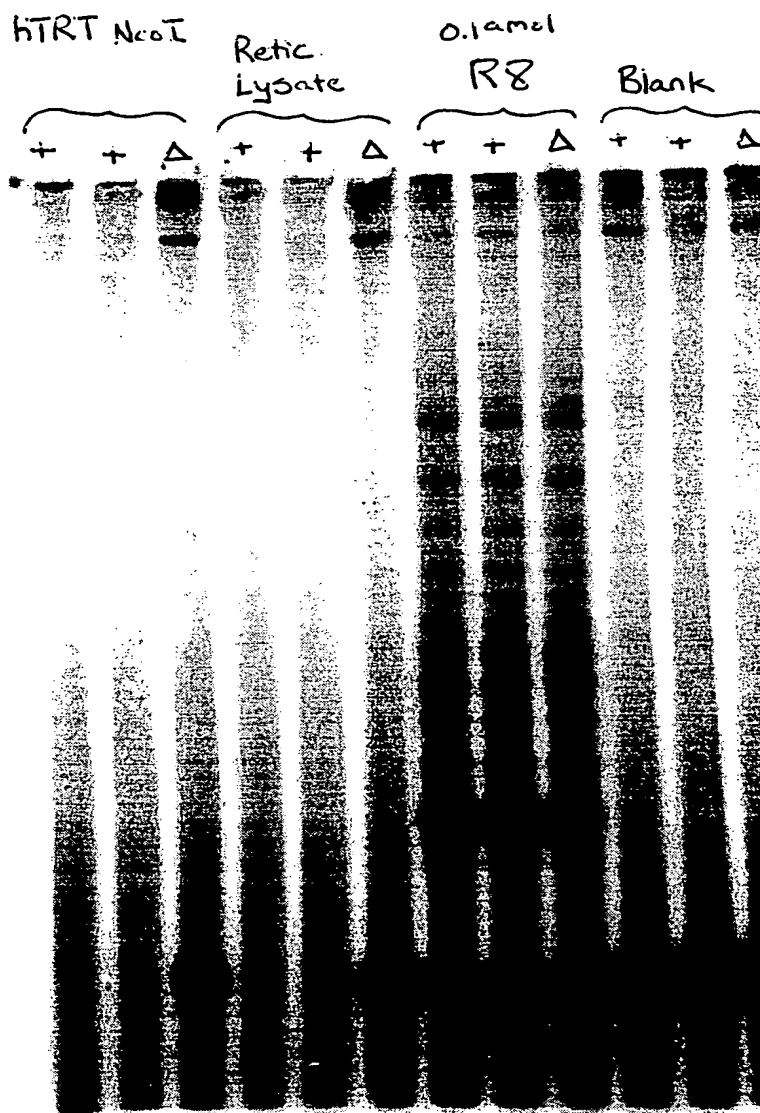


Figure 10
Page 1



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Figure 10
Page 2



08912951.081497

FIGURE 11.

Page 1

Telomerase Specific Motifs

	MOTIF T	MOTIF T'
TRT con	Wl	
hTRT	FFY TE	E V
spTRT	Y Rk W l I	EAEVR
Ea_p123	546 WLMsVYVVELLRsFFYVTETTFQKNRLFFYRKSWSKLQSIGI 13	EAEVR
Sc_Est2	429 WLYNSFIIPILQsFFYITESDDLNRNRTVYFRKDIWKLICRPFI 12	ENNVr
	441 WIFEDLVSLIRCFYVTEQQKSYSKTYRKNIDVIMKMSI 12	EKEVE
	366 WLFRLIPKIIQTFFYCTEISSTVT.IVYFRHDTWNKLITPFI 9	ENNVc

Telomerase RT Motifs (Fingers)

	MOTIF 1	MOTIF 2	MOTIF A		MOTIF B'	
	R ipKk	fr I	p lyF	D	cyD i	Y q GIPQGs lS l
TRT con						
hTRT	11 SRLRFIPKPDG 0 LRPIV		69 PELYFVKVDVTGAYDTI	104	YVQCQGIPOGSILSTLLCSLCY	
spTRT	10 AVIRLLPKKNT 0 FRLIT		66 RKKYFVRIDIKSCYDRI	99	YLQKVGIPOGSILSSFLCHFYM	
Ea_p123	10 GKLRLIPKKT 0 FRPIM		67 PKLFFATMDIEKCYDSV	117	YKQTKGIPQGLCVSSILSSFY	
Sc_Est2	13 SKMRIIPKKS 2 FRIIA		68 PELYFMKFDVKSCYDSI	85	YIREDGLFQGSLSAPIVDLVY	
RT con	p hh h K	hr h	h	hDh	AF h	hPQG pp hh h
						GY

FIGURE 11
Page 2

Telomerase RT Motifs (Palm, Primer Grip)

	MOTIF C	MOTIF D	MOTIF E	
TRT con	111rl DDfL it	g n K	w g s l	
hTRT	15 LLLRLVDDFLLVT	15 GVPEYGCVVNLRKTVV	24 WCGLLLDTRTL	192
spTRT	16 VLLRVVDDFLFIT	15 GFEKHNFSLEKTVI	22 FFGFSVNMRS L	176
Ea_p123	24 LLMRLTDDYLLIT	15 VSRENGFKFNMKKLQT	28 WIGISIDMKTL	174
Sc_Est2	18 LILKLADDFLIIS	15 GFQKYNAPANRDKILA	25 WKHSSTMNNFH	141
RT con	h Y DDhhh	Gh h cK h	hLG h	
	F			

FIGURE 12

181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC
CCTGGGCCGCGCGAAAGGCGCGGACCACCGGGTCACGGACCACACGCACGGGACCCTGCG

NFkB_CS1
GGGRQTYYYQC
NFkB-MHC-I.2
TGGGCTTCCCC

241 ACGGCCGCCCCCGCGCCCCCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCG
TGCCGGCGGGGGGCGGCGGGGGAGGAAGGCGGTCCACCCGAGGGGCCCCAGCCGCAGGC

Intron1

301 GCTGGGGTTGAGGGCGGCCGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTC
CGACCCCAACTCCCGCCGCCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

NFkB_CS1
GGGRQTYYYQC
NFkB_CS2
RGGGRMTYYCC

Topo_II_cleavage_site
RNYNNCNNGYNGKTNINY

*****>

361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGG
TCCCGCGAAGGGGGCGTCCACAGGACGGAATTCTCGACCACCGGGCTCACGACGTCTCC

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Figure 13

Page 1

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTAAGTACAGC
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
251 TTAGAAGATA TTAATAATATT TGCAGCAGACA AATATTGTTG CTACTCCACG
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAAGTTCTT
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
501 CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT
901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
1051 TCCTCTTCCA GAAAATTGGC GGAACGGAA AAAAAAATC GAAAAGTTGA
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151 TACACAAGT ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTT
1251 AAAAGAAAGT TAAGAAATAT GTGGAAGTAA ACAAGCATGA ACTCATTAC
1301 AAAAAGTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GGTGAGACC TCTGCAAGC ATTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451 CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701 TAAATTCAGA CCGGAAGACT ACAAATTAAT CTACAAATAC GAAGTTATTG
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851 AGTTTGTGTTG CAAATGGAAG CAAGTTGGAC AACCAAACT CTTCTTTGCA
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAAGTATC
1951 AACATTCTTA AAAAGTACTA AATTACTTTC TTAAGATTTT TGGATTATGA
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101 TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTG CTTGAAAATG
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
2251 CCAATATAAT TACATTAAGT TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT

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Figure 13

Page 2

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACCTCT
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201 CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTTG TCTTATATAC
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

264TBD" 1552T580

Figure 14

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVVRAM
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGGA
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNMKSRTTR IFYCTHFNRN
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAM
301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYEEELFS
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELH
401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWT FEDLVVS
451 LIRCFYVTE QQKSYSKTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
501 EEWKKS LGFA PGKLR LIPKK TTFRPIMTFN KKIVNSDRKT TKLTNTKLL
551 NSHLM LKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNVIDSKN
651 FRKKEMKD YF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKT LIVEAKQ
701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFY
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVL FIEKL
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
851 SIDMKTALM PNINLRIEGL CTLNLNMQT KKASMWLKKK LKSFLMNNIT
901 HYFRKTTTTE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID
951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
1001 KYTFNRVCM I LKAKEAKLKS DQCQSLIQYD A

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Figure 15

Page 1

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1 ggtaccgattttacttttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga 80
81 actcaataacaataaccaagtcaaattccaatatgaagggtgttatttagtgatcgataaatatttctattttatcggtcgta 160
161 ccaagtataaggacaaaaagaacaacttccttccccctaaagacttttactttattaatttacttttcaaataatatttcg 240
241 ggttcgcttacttttaacgtggtactgttttagctgctacttctagccaaccgctgtttctaccccgctcattggatat 320
321 agctcttggagtagctcacagaaatccttacaatcttctgatgagactatattagattcattacagtcctgcatattc 400
401 ttaacatggagccttacacttttagatgagtcacgtcgcgatgatggagtatttgggtatcatccaacgcttgacctgaaaag 480
481 gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagttttttgatgcttgcacacgtctagcatg 560
561 attgagatattcaaaaatttctatccactacaactcctttaacgcggtttttatttttctattttctattctcatgttggt 640
641 ccaaatatgtatcatctcgtatttaggcttttttccggttttactcctggaatcgtacctttttcactattccccctaata 720
721 ataactctaaatttagtttcgcttataattgatagtagtagaaaagatttgggtgattctactcgtgtaattgttattagtttaa 800
801 gatactttgcaaaacatttatttagctatcattatataaaaaaaatcctataattataaaatattaatcaatatttgcggtc 880
881 actattttatttaaaacggttatgatcagtaggacactttgcatatatatagtttatgcttaacggttacttgtaacttgc 958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
    1 M  T  E  H  H  T  P  K  S  R  I  L  R  F  L  E  N  Q  Y  V  20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
    21 Y  L  C  T  L  N  D  Y  V  Q  L  V  L  R  G  S  P  A  S  S  40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
    41 Y  S  N  I  C  E  R  L  R  S  D  V  Q  T  S  F  S  I  F  L  60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
    61 H  S  T  V  V  G  F  D  S  K  P  D  E  G  V  Q  F  S  S  P  80

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Figure 15

Page 2

1199 AAA TGC TCA CAG TCA GAG gtatatatatattttgttttgattttttttctatttcgggatagctaatatatgggcag 1272
81 K C S Q S E 86

1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA 1332
87 L I A N V V K Q M F D E S F E R R R N L 106

1333 CTG ATG AAA GGG TTT TCC ATG gtaagggtatttctaattgtgaaatattttacctgcaattactgttttcaaagaga 1405
107 L M K G F S M 113

1406 ttgtattttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT 1469
114 N H E D F R A M H V N G V Q N 128

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
129 D L V S T F P N Y L I S I L E S K N W Q 148

1530 CTT TTG TTA GAA AT gtaaataaccgggttaagatgttgcgacattttgaacaagactgacaagtatag T ATC GGC 1601
149 L L L E I I G 155

1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
156 S D A M H Y L L S K G S I F E A L P N D 175

1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
176 N Y L Q I S G I P L F K N N V F E E T V 195

1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781
196 S K K R K R T I E T S I T Q N K S A R K 215

1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
216 E V S W N S I S I S R F S I F Y R S S Y 235

1842 AAG AAG TTT AAG CAA G gtaactaataactgttatcccttcataactaatttttag AT CTA TAT TTT AAC 1907

236 K K F K Q D L Y F N 245

1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
246 L H S I C D R N T V H M W L Q W I F P R 265

1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027
266 Q F G L I N A F Q V K Q L H K V I P L V 285

2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
286 S Q S T V V P K R L L K V Y P L I E Q T 305

2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
306 A K R L H R I S L S K V Y N H Y C P Y I 325

2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
326 D T H D D E K I L S Y S L K P N Q V F A 345

2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267
346 F L R S I L V R V F P K L I W G N Q R I 365

2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaaattttattaccactaaccgattttaccag AC CTC GAA ACT 2336
366 F E I I L K D L E T 375

Figure 15

Page 3

2337	TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG	2396
376	F L K L S R Y E S F S L H Y L M S N I K	395
2397	gtaatatgccaaatttttttaccattaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA	2465
396	I S E I E W L V L G	405
2466	AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG	2525
406	K R S N A K M C L S D F E K R K Q I F A	425
2526	GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT	2585
426	E F I Y W L Y N S F I I P I L Q S F F Y	445
2586	ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA	2645
446	I T E S S D L R N R T V Y F R K D I W K	465
2646	CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA -ATA AAC GAG	2705
466	L L C R P F I T S M K M E A F E K I N E	485
2706	gtatttttaaagtatttttttgcaaaaagctaataattttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT	2775
486	N N V R M D T Q K T	495
2776	ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG	2835
496	T L P P A V I R L L P K K N T F R L I T	515
2836	AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaatttttggatcatcaatgtactttactttctaattctatta	2906
516	N L R K R F L I K	524
2907	ctagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG	2967
525	M G S N K K M L V S T N Q T L R P V	542
2968	GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG	3027
543	A S I L K H L I N E E S S G I P F N L E	562
3028	GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat	3088
563	V Y M K L L T F K K D L L K H R M F G	581
3089	tatataatgcgcgattccctcattattaatttttgcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA	3155
582	R K K Y F V R I D I	591
3156	AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC	3215
592	K S C Y D R I K Q D L M F R I V K K K L	611
3216	AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT	3275
612	K D P E F V I R K Y A T I H A T S D R A	631
3276	ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagttttatttttttcattggaatttttttaacaa	3343
632	T K N F V S E A F S Y F	643
3344	atttttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA	3405
644	D M V P F E K V V Q L L S M K T	659
3406	TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT	3465
660	S D T L F V D F V D Y W T K S S S E I F	679
3466	AAA ATG CTC AAG GAA CAT CTC TCT CGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca	3532
680	K M L K E H L S G H I V K	692

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Figure 15

Page 4

3533	ctaataaactag	ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA	3593
693		I G N S Q Y L Q K V G I P Q G S	708
3594	ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG	3653	
709	I L S S F L C H F Y M E D L I D E Y L S	728	
3654	TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA	3713	
729	F T K K K G S V L L R V V D D F L F I T	748	
3714	GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtagagttgctgctcattcc	3777	
749	V N K K D A K K F L N L S L R G	764	
3778	taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA	3840	
765	F E K H N F S T S L E K T V	778	
3841	ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA	3900	
779	I N F E N S N G I I N N T F F N E S K K	798	
3901	AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT	3960	
799	R M P F F G F S V N M R S L D T L L A C	818	
3961	CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG	4020	
819	P K I D E A L F N S T S V E L T K H M G	838	
4021	AAA TCT TTT TTT TAC AAA ATT CTA AG gtataactgtgtaactgaataatagctgacaaataatcag A TCG	4089	
839	K S F F Y K I L R	848	
4090	AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT	4149	
849	S L A S F A Q V F I D I T H N S K F N S	868	
4150	TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA	4209	
869	C C N I Y R L G Y S M C M R A Q A Y L K	888	
4210	AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtagagtacttattttaactaga	4274	
889	R M K D I F I P Q R M F I T D	903	
4275	aaagtcattaattaaccccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC	4339	
904	L L N V I G R K I W K K L A	917	
4340	GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc	4401	
918	E I L G Y T S R R F L S S A E V K W	935	
4402	gggtctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA	4468	
936	L F C L G M R D G L K	946	
4469	CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT	4528	
947	P S F K Y H P C F E Q L I Y Q F Q S L T	966	
4529	GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA	4588	
967	D L I K P L R P V L R Q V L F L H R R I	986	
4589	GCT GAT TAA tgtcattttcaatttattatatacatcctttattactgggtgtcttaaacatattattactaagtata	4665	
987	A D	989	

464791 1561251 081497

Figure 15
Page 5

4666 gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagcttttgattgacttgtct 4745
4746 ttatcctttatactttttaagaaagattgacagtgggttgctgactactgcccacatgcccattaaacgggagtggttaaaca 4825
4826 ttaaaagtaatacatgaggctaactctcctttcatttagaataaggaaagtgggttttctataatgaataatgcccgcacta 4905
4906 atgcaaaaagacgaagattatcttctaaacaaggggggattaagcatatccgaaggaaaagagagtaacatacccagtgtt 4985
4986 gctgaagaaagcaaggataaatttggaacaagcttctgcagatgacaggctaataatttggtgaccgaattttggtaaaagc 5065
5066 cccagggttatccatgggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaataactaatagctcattta 5145
5146 atgtcttatataagggttttggttttttccctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305
5306 tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgc 5385
5386 aaaaaagaaaatattcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata 5465
5466 acctctatttctgaaatgtatggctcctactgtcgcttcgacttctcgtagctctacgcagcttaagtgaccaaaggtacc 5544

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FIGURE 16
page 1
(Seq. ID. No. 1)

1 gcagcgctgc gtectgctgc gcacgtggga agccctggcc ccggccaccc ccgcgatgcc
61 gcgcgctccc cgctgccgag ccgtgcgctc cctgctgcgc agccactacc gcgaggtgct
121 gccgctggcc acgttcgtgc ggcgccctggg gccccagggc tggcggtgg tgcagcgcg
181 ggacccggcg gctttccgcg cgctggtggc ccagtgcctg gtgtgcgtgc cctgggacgc
241 acggccgccc ccgcccgc cctccttccg ccaggtgtcc tgctgaagg agctgggtggc
301 ccgagtgtcg cagaggctgt gcgagcgcg cgcaagaac gtgctggcct tcggcttcgc
361 gctgctggac gggggccgcg gggggccccc cgaggccttc accaccagcg tgcgcagcta
421 cctgcccac acggtgaccg acgactgcg ggggagcggg gcgtgggggc tgctgctgcg
481 ccgctggggc gacgacgtgc tggttcacct gctggcacgc tgcgcgctct ttgtgctggt
541 ggctcccagc tgcgcctacc aggtgtgcgg gccgcccgtg taccagctcg gcgctgccac
601 tcaggcccg ccgccgccac acgctagtgg accccgaagg cgtctgggat gcgaacgggc
661 ctggaacat agcgtcaggg aggcgggggt cccctggggc ctgccagccc cgggtgcgag
721 gaggcgcggg ggcagtgcc a gccgaagtct gccgttgccc aagaggccca ggcgtggcg
781 tgccctgag ccggagcgga cgcccgttg gccaggggtcc tggggccacc cgggcaggac
841 gcgtggaccg agtgaccgtg gtttctgtgt ggtgtcacct gccagaccgc ccgaagaagc
901 cacctctttg gaggggtgcg tctctggcac gcgccactcc caccatccg tgggccgcca
961 gcaccacgcg gggcccccat ccacatcgcg gccaccacgt ccctgggaca cgccttgtcc
1021 cccggtgtac gccgagacca agcacttct ctactcctca ggcgacaagg agcagctgcg
1081 gccctccttc ctactcagct ctctgaggcc cagcctgact ggcgtcgga ggctcgtgga
1141 gaccatcttt ctgggttcca ggccctggat gccagggact cccgcaggt tgccccgcct
1201 gccccagcgc tactggcaaa tgcggccct gtttctggag ctgcttggga accacgcgca
1261 gtgcccctac ggggtgctcc tcaagacgca ctgcccgtg cgagctgcgg tcacccagc
1321 agccggtgtc tgtgcccggg agaagcccca gggctctgtg gcggccccc aggaggagga
1381 cacagacccc cgctgcctgg tgcagctgct ccgccagcac agcagccctt ggcaggtgta
1441 cggtctcgtg cgggcctgcc tgcgcccgt ggtgccccca ggctctggg gctccaggca
1501 caacgaacgc cgcttctca ggaacaccaa gaagttcatc tcctgggga agcatgccaa
1561 gctctcgtg caggagctga cgtggaagat gagcgtgcgg gactgcgctt ggctgcgag
1621 gagcccagg gttggctgtg ttccggccgc agagcacctg ctgctgagg agatcctggc
1681 caagttcctg cactggctga tgagtgtgta cgtcgtcgag ctgctcaggt ctttctttta
1741 tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag
1801 caagttgcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggagctgtc
1861 ggaagcagag gtcaggcagc atcggaagc caggcccgcc ctgctgacgt ccagactccg
1921 cttcatcccc aagcctgacg ggctgcggcc gattgtgaac atggactacg tcgtgggagc
1981 cagaacgttc cgcagagaaa agagggccga gcgtctcacc tcgaggggtga aggcactgtt
2041 cagcgtgctc aactacgagc gggcgcgcg ccccggcctc ctgggcgcct ctgtgctggg
2101 cctggacgat atccacagg cctggcgcac cttcgtgctg cgtgtgcggg cccaggaccc
2161 gccgctgag ctgtactttg tcaaggtgga tgtgacgggc gcgtacgaca ccacccccca
2221 ggacaggctc acggaggtca tcgccagcat catcaaacc cagaacacgt actgcgtgcg
2281 tcggtatgcc gtggtccaga aggcgcgcca tgggcacgtc cgcaaggcct tcaagagcca
2341 cgtctctacc ttgacagacc tccagccgta catgacagag ttcgtggctc acctgcagga
2401 gaccagccc ctgagggat ccgtcgtcat cgagcagagc tcctccctga atgaggccag
2461 cagtggcctc ttgcagctc tctacgctt catgtgccac cagccgtgc gcacagggg
2521 caagtcctac gtccagtgc aggggacccc gcagggtcc atcctctcca cgtgctctg
2581 cagcctgtgc taggcgaca tggagaacaa gctgtttgcg gggattcggc gggacgggg
2641 gctcctgctg ttggtggatg atttcttgtt ggtgacacct cacctaccc acgcgaaaac
2701 cttcctcagg accctggctc gaggtgtccc tgagtatggc tgcgtgggtga acttgcgga
2761 gacagtgggtg aacttccctg tagaagacga ggccctgggt ggcacggctt ttgttcagat
2821 gccggccccc ggccatttcc cctggtgcgg cctgctgctg gatacccgga ccctggaggt
2881 gcagagcgac tactccagct atgcccggac ctccatcaga gccagttctc ccttcaaccg

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FIGURE 16
page 2
(Seq. ID. No. 1)

2941 cggcttcaag gctgggagga acatgcgtcg caaactcttt ggggtcttgc ggctgaagtg
3001 tcacagcctg tttctggatt tgcaggtgaa cagcctccag acggtgtgca ccaacatcta
3061 caagatcctc ctgctgcagg cgtacaggtt tcacgcatgt gtgctgcagc tcccatttca
3121 tcagcaagtt tgggaagaacc ccacattttt cctgcgcgtc atctctgaca cggcctccct
3181 ctgctactcc atcctgaaag ccaagaacgc agggatgtcg ctgggggcca agggcgccgc
3241 cggccctctg ccctccgagg ccgtgcagtg gctgtgccac caagcattcc tgctcaagct
3301 gactcgacac cgtgtcacct acgtgccact cctgggggtca ctcaggacag cccagacgca
3361 gctgagtcgg aagctcccgg ggacgacgct gactgccctg gaggccgcag ccaaccgggc
3421 actgccctca gacttcaaga ccatcctgga ctgatggcca cccgcccaca gccaggccga
3481 gagcagacac cagcagccct gtcacgccgg gctctacgtc ccagggaggg agggcgggcc
3541 cacaccagg cccgcaccgc tgggagtctg aggcctgagt gagtgtttgg ccgaggcctg
3601 catgtccggc tgaaggctga gtgtccggct gaggcctgag cgagtgtcca gccaaaggct
3661 gagtgtccag cacacctgcc gtcttcaact cccacaggc tggcgctcgg ctccacccca
3721 gggccagctt ttctcacca ggagcccggc ttccactccc cacataggaa tagtccatcc
3781 ccagattcgc cattgttcac ccctcgccct gccctccttt gccttccacc cccaccatcc
3841 aggtggagac cctgagaagg accctgggag ctctgggaat ttggagtgac caaagggtgtg
3901 ccctgtacac aggcgaggac cctgcacctg gatgggggtc cctgtgggtc aaattggggg
3961 gaggtgctgt gggagtaaaa tactgaatat atgagttttt cagttttgaa aaaaa

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FIGURE 17
HUMAN TRT PROTEIN SEQUENCE
(SEQ. NO. 2)

MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDP
AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFA
LLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFV
LVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPA
PGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPA
RPAAEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYS
SGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPL
FLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPGQSVAAPEEEDTDPRRLVQ
LLRQHSSPWQVYGFVRACLRRLLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQEL
TWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTET
TFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFI
PKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLG
LDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYC
VRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSL
NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGD MENKLFAG
IRR DGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFVVEDEAL
GGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRR
KLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQVWKNPT
FFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLCLKLTRHRT
YVPLLGSRLRTAQTQLSRKLP GTTLTALEAAANPALPSDFKTILD

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FIGURE 18
Clone 712562
(SEQ ID NO. 3)

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT
TTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTG
GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGACAGCTGCGGGAGCT
GTCGGAAGCAGAGGT CAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACT
CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGG
AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT
GTT CAGCGTGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGCGCCTCTGTGCT
GGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGGCCAGGA
CCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCC
CCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGT
GCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAG
CCACGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT
GCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTTCGGCGGGACGGGC
TGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAA
CCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGCGGA
AGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT CAGA
TGCCGGCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGG
TGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACC
GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTTGGGGTCTTGCGGCTGAAGT
GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT
ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCCATTTT
ATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCC
TCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCG
CCGGCC7TCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGC
TGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGC
AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCCAACCCGG
CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCG
AGAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCAGGGAGGGAGGGGCGGC
CCACACCCAGGCCTGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCT
GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC
TGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCACAGGCTGGCGCTCGGCTCCACCCC
AGGGCCAGCTTTTCTCACCAGGAGCCGGCTTCCACTCCCCACATAGGAATAGTCCATC
CCCAGATTCGCCATTGTTTCAACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATC
CAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGT
GCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGG
GGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTG0AAAAAAAAA
AAAAAAAAAAAAAAAAA

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FIGURE 19

SEQ ID NO. 10

MetSerValTyrValValGluLeuLeuArgSerPhePhe
TyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrp
SerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeu
SerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeu
ArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGly
AlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeu
PheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeu
GlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAsp
ProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIlePro
GlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysVal
ArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSer
HisValLeuArgProValProGlyAspProAlaGlyLeuHisProLeuHisAlaAlaLeu
GlnProValLeuArgArgHisGlyGluGlnAlaValCysGlyAspSerAlaGlyArgAla
AlaProAlaPheGlyGly

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Page 1

SECRET

met

10

20

30

40

50

60

70

80

90

100

110

120

ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

FIGURE 20

Page 2

130

tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

140

150

trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

160

leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

170

180

ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

190

thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

200

210

leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

220

val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230

240

ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

250

ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

260

270

ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

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FIGURE 20

Page 3

280

val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

290

300

gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310

gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320

330

trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340

leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350

360

leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370

glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380

390

arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400

leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410

420

val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430

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Page 4

ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440

450

ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460

leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470

480

ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490

his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500

510

leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520

met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CCG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530

540

gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550

ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560

570

leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580

arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

[illegible]

FIGURE 20

Page 5

590 600
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
 pro ile val asn met asp tyr val val gly ala arg thr phe arg
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
 TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
 thr phe val leu arg val arg ala gln asp pro pro pro glu leu
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720
 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

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FIGURE 20

Page 6

740

asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

750

760

his gly his val arg lys ala phe lys ser his val leu arg pro
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

770

val pro gly asp pro ala gly leu his pro leu his ala ala leu
GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

780

790

gln pro val leu arg arg his gly glu gln ala val cys gly asp
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

800

807

ser ala gly arg ala ala pro ala phe gly gly OP
TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTGGT

GACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA
GTATGGCTGCGTGGTGAACCTTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGC
CCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCCCTGGTGCGGCCT
GCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC
CATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAA
ACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAG
CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA
CGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGGAAGAACCCACATTTTTCCT
GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG
GATGTCGCTGGGGGCCAAGGGCGCCGCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCT
GTGCCACCAAGCATTCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCT

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FIGURE 20

Page 7

GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC
TGCCCTGGAGGCCGCGAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG
ATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTCACGCCGGGCT
CTACGTCCCAGGGAGGGAGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG
CCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCGGGCTGAG
GCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTCAGCACACCTGCCGTCTTCACTTCCC
CACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTC
CACTCCCCACATAGGAATAGTCCATCCCCAGATTGCGCCATTGTTTACCCCTCGCCCTGCC
CTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTC
TGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT
GGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATG
AGTTTTTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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page 1

3601 ATCGATTGGGCCCCGAGATCTCGCGCGCGAGGCCTGCCATGGGACCCACTGCAGGGGCGAGC
TAGCTAACCCGGGCTCTAGAGCGCGCGCTCCGGACGGTACCCTGGGTGACGTCCCCGTCTG

3636
NCO1

4201 TGCCTCTGCCTCCTAAAATTGCTGGGATTACAGGTGTNANCCACCATGCCCAACTCAAAA

FIGURE 21

page 2

ACGGAGACGGAGGATTTTAACGACCCTAATGTCCACANTNGGTGGTACGGGTTGAGTTTT

4261 TTTACTCTGTTTANAAACATCTGGGTCTAAGGTAGGAANCTCACCCCACTCAATTTTTGT
AAATGAGACAAATNTTTGTAGACCCAGATTCCATCCTTNGAGTGGGGTGAGTTAAAAACA

4321 GGTGTTTTTAAGCCAATNANAAAATTTTTTNATGTTGTTTNNNNNNNNNNNNNNNNNNNN
CCACAAAATTCGGTTANTNTTTTAAAAAANTACAACAAANNNNNNNNNNNNNNNNNNNN

4381 NNN
NN

4441 NNN
NN

4501 NNN
NN

4561 NNN
NN

4621 NNN
NN

4681 NNN
NN

4741 NNN
NN

4801 NNN
NN

4861 NNN
NN

4921 NNN
NN

4981 NNN
NN

5041 NGCCANGRAGGGGGCCAGGTTCCAANTTCCCAACCKTTTTWGGARGGACNGCCCCCAGGG
NCGGTNCYTCCCCCGGTCCAAGGTTNAAGGGTTGGMAAAWCCCTYCCTGNCGGGGGTCCC

5101 GGGGATRAACAGANTNGGGGGKGGTWGGGTTNAKGGTGGGAACNCCTTNGCGCCTGGAG
CCCCTAYTTGTCTNANCCCCMCCAWCCCAANTMCCACCCTTGNGGAANCGSCGGACCTC

5161 AACGTGCAAAGAGGAAATGAAGGGCCTGKGTCAAGGAGCCCAAGTNGGCGGGGRAGTTTG
TTGCACGTTTCTCCTTTACTTCCCGGACMCAGTTCCTCGGGTTCANCCGCCCCYTCAAAC

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FIGURE 21

page 3

5221 CAGGGAGGCACTCCGGGGAGGTCCSGCGTGCCCGTCCAAGGGAGCAATGCGTCCTTCGGG
GTCCCTCCGTGAGGCCCTCCAGGSCGCACGGGCAGGTTCCCTCGTTACGCAGGAAGCCC

5281 TTCGTCCCCAWGCCGCGTCTACGCGCCTYCCGTCTCCCTTCACGTTCCGGCATTTCGTG
AAGCAGGGGTWCGGCGCAGATGCGCGGARGGCAGGAGGGGAAGTGCAAGGCCGTAAGCAC

5341 GTGCCCCGAGCCCCGACGCCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGATCAG
CACGGGCCTCGGGCTGCGGGGCGCAGGCCCTGGACCTCCGTGCGGGACCCAGAGGCCTAGTC

5401 GCCAGCGGCCAAAGGGTCGCGGCACGCACCTGTTCCAGGGCCTCCACATCATGGCCCCCT
CGGTGCGCCGTTTCCAGCGGCGTTCGTGGACAAGGGTCCCGGAGGTGTAGTACCGGGGA

5461 CCCTCGGGTTACCCACAGCCTAGGCCGATTTCGACCTCTCTCCGCTGGGGCCCTCGCCT
GGGAGCCCAATGGGGTGTTCGATCCGGCCTAAGCTGGAGAGAGGCGACCCGGGAGCGGA

Sp1

5521 GCGTCCCTGCACCCTGGGAGCGCGAGCGGCGCGGGCGGGGAAGCGCGGCCCATACCC
CCGCAGGGACGTGGGACCCTCGCGCTCGCCGCGCGCCCGCCCTTCGCGCCGGGTATGGG

5581 CCGGGTCCGCCCCGAAGCAGCTGCGCTGTGCGGGCCAGGCCGGGCTCCAGTGGATTTCG
GGCCAGGCGGGCCTTCGTGACGCGACAGCCCCGGTCCGGCCCGAGGGTCACCTAAGCG

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5641 GGGCACAGACGCCCAGGACCGCGCTTCCACGTGGCGGAAGGACTGGGGACCCGGGCACC
CCCGTGTCTGCGGGTCTGGCGCGAAGGGTGACCGCCTTCCTGACCCCTGGGCCCCGTGG

E2F

5701 CGTCCTGCCCCCTTCACCTTCCAGCTCCGCTTCTTCCGCGCGGACCCGGCCCCGTCCCGAA
GCAGGACGGGGAAGTGGAAGGTCGAGGCGAAGAAGGCGCGCCTGGGCGGGGCAGGGCTT

E

5761 CCCTTCCCAGGTCCCGGCCAGCCCCCTTCGGGGCCCTCCAGCCCCCTCCCTTCTTTT
GGGAAGGGTCCAGGGCCGGGTGCGGGGAAGGCCGGGAGGGTCGGGGAGGGGAAGGAAAAG

0841521541551561571581591601611621631641651661671681691701711721731741751761771781791801811821831841851861871881891901911921931941951961971981992002012022032042052062072082092102112122132142152162172182192202212222232242252262272282292302312322332342352362372382392402412422432442452462472482492502512522532542552562572582592602612622632642652662672682692702712722732742752762772782792802812822832842852862872882892902912922932942952962972982993003013023033043053063073083093103113123133143153163173183193203213223233243253263273283293303313323333343353363373383393403413423433443453463473483493503513523533543553563573583593603613623633643653663673683693703713723733743753763773783793803813823833843853863873883893903913923933943953963973983994004014024034044054064074084094104114124134144154164174184194204214224234244254264274284294304314324334344354364374384394404414424434444454464474484494504514524534544554564574584594604614624634644654664674684694704714724734744754764774784794804814824834844854864874884894904914924934944954964974984995005015025035045055065075085095105115125135145155165175185195205215225235245255265275285295305315325335345355365375385395405415425435445455465475485495505515525535545555565575585595605615625635645655665675685695705715725735745755765775785795805815825835845855865875885895905915925935945955965975985996006016026036046056066076086096106116126136146156166176186196206216226236246256266276286296306316326336346356366376386396406416426436446456466476486496506516526536546556566576586596606616626636646656666676686696706716726736746756766776786796806816826836846856866876886896906916926936946956966976986997007017027037047057067077087097107117127137147157167177187197207217227237247257267277287297307317327337347357367377387397407417427437447457467477487497507517527537547557567577587597607617627637647657667677687697707717727737747757767777787797807817827837847857867877887897907917927937947957967977987998008018028038048058068078088098108118128138148158168178188198208218228238248258268278288298308318328338348358368378388398408418428438448458468478488498508518528538548558568578588598608618628638648658668678688698708718728738748758768778788798808818828838848858868878888898908918928938948958968978988999009019029039049059069079089099109119129139149159169179189199209219229239249259269279289299309319329339349359369379389399409419429439449459469479489499509519529539549559569579589599609619629639649659669679689699709719729739749759769779789799809819829839849859869879889899909919929939949959969979989991000100110021003100410051006100710081009101010111012101310141015101610171018101910201021102210231024102510261027102810291030103110321033103410351036103710381039104010411042104310441045104610471048104910501051105210531054105510561057105810591060106110621063106410651066106710681069107010711072107310741075107610771078107910801081108210831084108510861087108810891090109110921093109410951096109710981099110011011102110311041105110611071108110911101111111211131114111511161117111811191120112111221123112411251126112711281129113011311132113311341135113611371138113911401141114211431144114511461147114811491150115111521153115411551156115711581159116011611162116311641165116611671168116911701171117211731174117511761177117811791180118111821183118411851186118711881189119011911192119311941195119611971198119912001201120212031204120512061207120812091210121112121213121412151216121712181219122012211222122312241225122612271228122912301231123212331234123512361237123812391240124112421243124412451246124712481249125012511252125312541255125612571258125912601261126212631264126512661267126812691270127112721273127412751276127712781279128012811282128312841285128612871288128912901291129212931294129512961297129812991300130113021303130413051306130713081309131013111312131313141315131613171318131913201321132213231324132513261327132813291330133113321333133413351336133713381339134013411342134313441345134613471348134913501351135213531354135513561357135813591360136113621363136413651366136713681369137013711372137313741375137613771378137913801381138213831384138513861387138813891390139113921393139413951396139713981399140014011402140314041405140614071408140914101411141214131414141514161417141814191420142114221423142414251426142714281429143014311432143314341435143614371438143914401441144214431444144514461447144814491450145114521453145414551456145714581459146014611462146314641465146614671468146914701471147214731474147514761477147814791480148114821483148414851486148714881489149014911492149314941495149614971498149915001501150215031504150515061507150815091510151115121513151415151516151715181519152015211522152315241525152615271528152915301531153215331534153515361537153815391540154115421543154415451546154715481549155015511552155315541555155615571558155915601561156215631564156515661567156815691570157115721573157415751576157715781579158015811582158315841585158615871588158915901591159215931594159515961597159815991600160116021603160416051606160716081609161016111612161316141615161616171618161916201621162216231624162516261627162816291630163116321633163416351636163716381639164016411642164316441645164616471648164916501651165216531654165516561657165816591660166116621663166416651666166716681669167016711672167316741675167616771678167916801681168216831684168516861687168816891690169116921693169416951696169716981699170017011702170317041705170617071708170917101711171217131714171517161717171817191720172117221723172417251726172717281729173017311732173317341735173617371738173917401741174217431744174517461747174817491750175117521753175417551756175717581759176017611762176317641765176617671768176917701771177217731774177517761777177817791780178117821783178417851786178717881789179017911792179317941795179617971798179918001801180218031804180518061807180818091810181118121813181418151816181718181819182018211822182318241825182618271828182918301831183218331834183518361837183818391840184118421843184418451846184718481849185018511852185318541855185618571858185918601861186218631864186518661867186818691870187118721873187418751876187718781879188018811882188318841885188618871888188918901891189218931894189518961897189818991900190119021903190419051906190719081909191019111912191319141915191619171918191919201921192219231924192519261927192819291930193119321933193419351936193719381939194019411942194319441945194619471948194919501951195219531954195519561957195819591960196119621963196419651966196719681969197019711972197319741975197619771978197919801981198219831984198519861987198819891990199119921993199419951996199719981999200020012002200320042005200620072008200920102011201220132014201520162017201820192020202120222023202420252026202720282029203020312032203320342035203620372038203920402041204220432044204520462047204820492050205120522053205420552056205720582059206020612062206320642065206620672068206920702071207220732074207520762077207820792080208120822083208420852086208720882089209020912092209320942095209620972098209921002101210221032104210521062107210821092110211121122113211421152116211721182119212021212122212321242125212621272128212921302131213221332134213521362137213821392140214121422143214421452146214721482149215021512152215321542155215621572158215921602161216221632164216521662167216821692170217121722173217421752176217721782179218021812182218321842185218621872188218921902191219221932194219521962197219821992200220122022203220422052206220722082209221022112212221322142215221622172218221922202221222222232224222522262227222822292230223122322233223422352236223722382239224022412242224322442245224622472248224922502251225222532254225522562257225822592260226122622263226422652266226722682269227022712272227322742275227622772278227922802281228222832284228522862287228822892290229122922293229422952296229722982299230023012302230323042305230623072308230923102311231223132314231523162317231823192320232123222323232423252326232723282329233023312332233323342335233623372338233923402341234223432344234523462347234823492350235123522353235423552356235723582359236023612362236323642365236623672368236923702371237223732374237523762377237823792380238123822383238423852386238723882389239023912392239323942395239623972398239924002401240224032404240524062407240824092410241124122413241424152416241724182419242024212422242324242425242624272428242924302431243224332434243524362437243824392440244124422443244424452446244724482449245024512452245324542455245624572458245924602461246224632464246524662467246824692470247124722473247424752476247724782479248024812482248324842485248624872488248924902491249224932494249524962497249824992500250125022503250425052506250725082509251025112512251325142515251625172518251925202521252225232524252525262527252825292530253125322533253425352536253725382539254025412542254325442545254625472548254925502551255225532554255525562557255825592560256125622563256425652566256725682569257025712572257325742575257625772578257925802581258225832584258525862587258825892590259125922593259425952596259725982599260026012602260326042605260626072608260926102611261226132614261526162617261826192620262126222623262426252626262726282629263026312632263326342635263626372638263926402641264226432644264526462647264826492650265126522653265426552656265726582659266026612662266326642665266626672668266926702671267226732674267526762677267826792680268126822683268426852686268726882689269026912692269326942695269626972698269927002701270227032704270527062707270827092710271127122713271427152716271727182719272027212722272327242725272627272728272927302731273227332734273527362737273827392740274127422743274427452746274727482749275027512752275327542755275627572758275927602761276227632764276527662767276827692770277127722773277427752776277727782779278027812782278327842785278627872788278927902791279227932794279527962797279827992800280128022803280428052806280728082809281028112812281328142815281628172818281928202821282228232824282528262827282828292830283128322833283428352836283728382839284028412842284328442845284628472848284928502851285228532854285528562857285828592860286128622863286428652866286728682869287028712872287328742875287628772878287928802881288228832884288528862887288828892890289128922893289428952896289728982899290029012902290329042905290629072908290929102911291229132914291529162917291829192920292129222923292429252926292729282929293029312932293329342935293629372938293929402941294229432944294529462947294829492950295129522953295429552956295729582959296029612962296329642965296629672968296929702971297229732974297529762977297829792980298129822983298429852986298729882989299029912992299329942995299629972998299930003001300230033004300530063007300830093010301130123013301430153016301730183019302030213022302330243025302630273028302930303031303230333034303530363037303830393040304130423043304430453046304730483049305030513052305330543055305630573058305930603061306230633064306530663067306830693070307130723073307430753076307730783079308030813082308330843085308630873088308930903

FIGURE 21

page 4

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5821 CGCGGCCCCGCCCTCTCCTTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCA
GCGCCGGGGCGGGAGAGGAAGCGCCGCGCTCAAAGTCCGTCGCGACGCAGGACGACGCGT

5860

ECO47III

5875

FSP1

TRT5'

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5881 CGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCCGCGCGCTCCCCGCTGCCGAGCCG
GCACCCTTCGGGACCGGGCCCGGTGGGGGCGCTACGGCGCGCGAGGGGCGACGGCTCGGC

5941 TGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCTGTCGGC
ACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGACGGCGACCGGTGCAAGCACGCCG

5953

FSP1

6001 GCCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGGGACCCGGCGGCTTTCCGCGCGC
CGGACCCCGGGGTCCCACCGCCGACACGTCGCGCCCCTGGGCGCGCGAAAGGCGCGC

6061 TGGTGGCCCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCCGCCCCCT
ACCACCGGGTCACGGACCACACGCACGGGACCCTGCGTGCCGGCGGGGGCGGCGGGGGA

NFkB

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6121 CCTTCCGCCAGGTGGGCCTCCCCGGGGTCCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGG
GGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGAGGCCGACCCAACTCCC GCCGGCCCC

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NFkB

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Intron1

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6181 GGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTGTC
CCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAGTCCCGCGAAGGGGGCGTCCACAG

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FIGURE 21

page 5

6241 CTGCCTGAAGGAGCTGGTGGCCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGGAAGAA
GACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTTCTT

6301 CGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGCCTT
GCACGACCGBAAGCCGAAGCGCGACGACCTGCCCCGGGCGCCCCGGGGGGGCTCCGGAA

6361 CACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGG
GTGGTGGTTCGACGCGTCGATGGACGGGTGTGCCACTGGCTGCGTGACGCCCCCTCGCC

6372

FSP1

6421 GGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACG
CCGCACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGGACGACCGTGC

6481 CTGCGCGCTCTTTGTGCTGGTGGCTCCAGCTGCGCCTACCAGGTGTGCGGGCCGCGCT
GACGCGCGAGAAACACGACCACCGAGGGTCGACGCGGATGGTCCACACGCCCGGCGGCGA

6541 GTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAG
CATGGTCGAGCCGCGACGGTGAGTCCGGGCGGGGGCGGTGTGCGATCACCTGGGGCTTC

6601 GCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGG
CGCAGACCTACGCTTGCCCGGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCC

6661 CCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGCGAGTGCCAGCCGAAGTCTGCCGTTGCC
GGACGGTCGGGGGCCACGCTCCTCCGCGCCCCCGTACGGTCGGCTTCAGACGGCAACGG

6721 CAAGAGGCCCGAGCGTGGCGCTGCCCCCTGAGCCGGAGCGGACGCCCCGTGGGCAGGGGTC
GTTCTCCGGGTCCGCACCGCGACGGGGACTCGGCCTCGCCTGCGGGCAACCCGTCCCCAG

6781 CTGGGCCCCACCGGGCAGGACGCGTGACCGAGTGACCGTGGTTTCTGTGTGGTGTACC
GACCCGGGTGGGCCCCGTCTGCGCACCTGGCTCACTGGCACCAAAGACACACCACAGTGG

6841 TGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTC
ACGGTCTGGGCGGCTTCTTCGGTGGAGAAACCTCCACGCGAGAGACCGTGCGCGGTGAG

6901 CCACCCATCCGTGGGCGGCCAGCACGCGGGCCCCCATCCACATCGCGGCCACCACG
GGTGGGTAGGCACCCGGCGGTTCGTGGTGCGCCCGGGGGTAGGTGTAGCGCCGGTGGTGC

6961 TCCCTGGGACACGCCTTGTCCCCGGGTGACGCCGAGACCAAGCACTTCCTCTACTCCTC
AGGGACCCTGTGCGGAACAGGGGGCCACATGCGGCTCTGGTTTCGTGAAGGAGATGAGGAG

7021 AGGCGACAAGGAGCAGCTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGAC
TCCGCTGTTCTCTGTCGACCGCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTCCGACTG

7081 TGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGGAC
ACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGTCCGGGACCTACGGTCCCTG

6372 FSP1

FIGURE 21

page 6

7141 TCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGCGGGCCCCTGTTTCTGGA
AGGGGCGTCCAACGGGGCGGACGGGGTCGCGATGACCGTTTACGCCGGGGACAAAGACCT

7167

ECO47III

7201 GCTGCTTGGGAACCACGCGCAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCCGCT
CGACGAACCCTTGGTGCGCGTCACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGGCGA

7261 GCGAGCTGCGGTACCCCCAGCAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGT
CGCTCGACGCCAGTGGGGTCTGTGCGCCACAGACACGGGCCCTCTTCGGGGTCCCAGACA

7321 GGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCA
CCGCCGGGGGCTCCTCCTCCTGTGTCTGGGGGCAGCGACCACGTCGACGAGGCGGTCTGT

7381 CAGCAGCCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCC
GTCGTGCGGGACCGTCCACATGCCGAAGCACGCCCGGACGGACGCGGCCGACCACGGGGG

7441 AGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCAT
TCCGGAGACCCCCAGGTCCGTGTTGCTTGCGGCGAAGGAGTCCTTGTGGTTCTTCAAGTA

7501 CTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCG
GAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCTCTGACTGCACCTTCTACTCGCACGC

7561 GGA CTGCGCTTGGCTGCGCAGGAGCCCAGGTGAGGAGGTGGTGCCGTCGAGGGCCCAGG
CCTGACGCGAACCAGCGCTCCTCGGGTCCACTCCTCCACCACCGGCAGCTCCCGGGTCC

7575

FSP1

Intron2

7621 CCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGGCAGGCAGAGCCCTGGTCCTCCT
GGGGTCTCGACTTACGTCATCCCCGAGTCTTTTCCCCCGTCCGTCTCGGGACCAGGAGGA

7681 GTCTCCATCGTCACGTGGGCACACGTGGCTTTTCGCTCAGGACGTGAGTGACACGGTG
CAGAGGTAGCAGTGACCCGTGTGCACCGAAAAGCGAGTCCTGCAGCTCACCTGTGCCAC

**>

7741 ATCGAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTTCGTAATCATGGTCATA
TAGCTCCAGCTGAGATCTCCTAGGGGCCCATGGCTCGAGCTTAAGCATTAGTACCAGTAT

7747

SAL1

000151.0340

FIGURE 23
EST AA281296
(Seq. ID. No. 8)

gc
caagttcctg cactggctga tgagtgtgta cgtcgtcgag ctgctcaggt ctttctttta
tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag
caagttgcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggacgtgtc
ggaagcagag gtcaggcagc atcggaagc caggcccgcc ctgctgacgt ccagactccg
cttcatcccc aagcctgacg ggctgcggcc gattgtgaac atggactacg tcgtgggagc
cagaacgttc cgcagagaaa agagggccga gcgtctcacc tcgaggggtga aggcactgtt
cagcgtgctc aactacgagc gggcgcg

08912961.081497

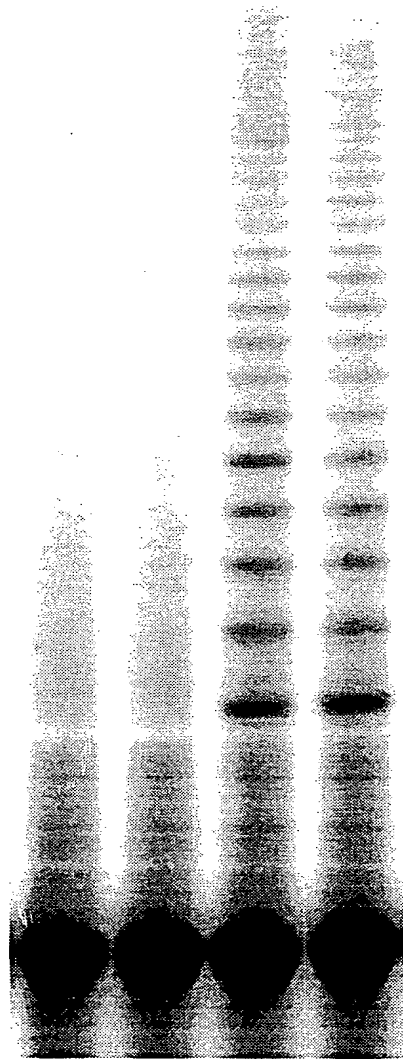
FIGURE 24
(Seq. ID. No. 9)

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG
ACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGC
CAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCAT
CAGGGGCAAGTC

0912551 081497
264780 15521580

Figure 25

pBBS212 pGRN133



← INTERNAL CONTROL

approximate cell # 5,000 5,000 5,000 5,000